

Abstract: Aldrovanda 2010

Organellar DNA from the widely distributed but rare and critically endangered aquatic carnivorous plant *Aldrovanda vesiculosa* (Droseraceae) was examined. Six chloroplast intergenic regions (3700 nt in total) were sequenced before analyzing the Southern-RFLP (Restriction Fragment Length Polymorphism) of 2 mt gene flanking regions. Only two different chloroplast haplotypes among 15 *A. vesiculosa* accessions from Africa, Australia, Europe, and Japan were found, generally distinguishing European and non-European plants, with two exceptions. Genetic variation observed in *A. vesiculosa* appears to be even lower than in other aquatic species with a similar world-wide distribution. A recent bottleneck followed by long-distance dispersal by water birds or low mutation rates could be responsible for the observed genetic uniformity. Estimation of genetic distances based on six chloroplast intergenic regions led to the conclusion that the chloroplast genome of *A. vesiculosa* matches more closely to that of *Drosera regia* than *Dionaea muscipula*, a sister genus sharing snapping traps. The inconsistency between genetic distance estimates based on nuclear and cytoplasmic markers may reflect a chloroplast capture. In *A. vesiculosa*, a four amino acids substitution (TGWS) in the amino acid sequence of ATP synthase alpha subunit (ATP1), highly conserved mitochondrial protein, was discovered, unique among all organisms based on current knowledge.